



**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application No.: 09/868,987

Applicant: MURDIN, Andrew D. et al.

Filed: December 23, 1999

TC/A.U.: 1645

Examiner: Padmavathi Baskar

Docket No: 032931/0253

**DECLARATION PURSUANT TO 37 CFR 1.131**

I, Andrew Murdin, Director, External R&D Canada, Aventis Pasteur, hereby declare that:

1. I am an inventor in the above-identified application, and am employed by the assignee, Aventis Pasteur.

2. Details of my employment history are as follows:

Since 2002 Director, External R&D Canada, Aventis Pasteur.

1999-2002 Principal Research Scientist, Aventis Pasteur.

1997-2002 Section Head, Aventis Pasteur.

1993-2003 Project Leader (Chlamydia), Aventis Pasteur.

1990-1993 Research Scientist, Connaught Laboratories Ltd. (subsequently Pasteur Merieux Connaught, subsequently Aventis Pasteur), Toronto, Canada.

1988-1990 Post-Doctoral Research Associate, Dept. of Microbiology, State University of New York, Stony Brook, NY, USA.

1985-1987 Post-Doctoral Research Fellow, Dept. of Microbiology, University of Surrey, Guildford, Surrey, England.

1981-1985 Scientific Officer, Vaccine Research Dept., Animal Virus Research Institute, Pirbright, Surrey, England.

Details of my education are as follows:

B.Sc., University of Bath, England, 1980

Ph.D., University of Surrey, England, 1986.

3. Attached is a copy of a document signed by me and Dathao Ho, an employee of the assignee Aventis Pasteur. The document sets forth the amino acid sequence, the nucleotide sequence, and the restriction map of CPN100686.

4. CPN100686 corresponds to the gene identified as SEQ ID Nos: 1 and 14 of the application. The amino acid sequence of CPN100686 set forth in the attached document is identical to SEQ ID No:14 of this application. The sequences and restriction map set forth in the document are essentially the same as those shown in Figures 1 and 14 of this application.

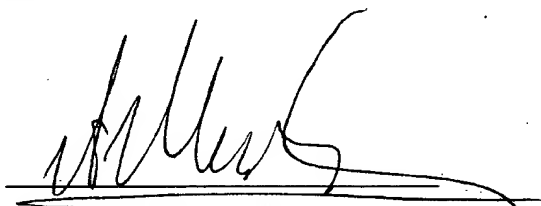
5. The dates deleted from the attached document are before November 4, 1998.

6. The document shows that I possessed these amino acid and nucleotide sequences prior to November 4, 1998.

7. I hereby declare that all statements made herein of my knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issuing thereon.

Mord 6<sup>th</sup> 2504

Date



Andrew Murdin

Director, External R&D Canada, Aventis Pasteur

**CONFIDENTIAL**

-CPN100686 protein-export membrane protein SecD  
 VSSPILNVPLKNHASVSGKFTTHREVSKLASDLKSGAMSFVPEVLSEETISDDLGGKQCTQGIIISACGLAMLIVL  
 MSVYYRVFGGVYIAGAVLLNLLLIWAALQYLDAPLTLSGLAGIVLAMGAVDANLVFERIREEFLLSQSLKKSVE  
 KGYYTAKFAGAI PDSNLTITVLASGLALFFLDTGPIKGFALTLILGIFSSMFTALFMTKFFFMLWMNKTHQHTQLHMMNK  
 FVGIKHDHDLRGCKKLWAVSGSVFLLCVAGLFGAWNSVLGMDFKGYAFTFNPKEHGISDVAQMRGKVVHKLQEA  
 GLSSRDHFRIQTPGSSEKIKIYFSDKSKFLYXSRYEPLSXNXRSXAGNVNGLLSETGLDFSTETLNQTNFWSKVS  
 SKLSKMMRYQATIGLLGALAILLYVSLRFEWQYAFSAVCALIHDLLATCAVLFI AHFFLKKI QIDLQAI GALMT  
 VLGYSLNLTLIIIFDRIREDRQANLFTPMHVLVNDALQKTF SRTVMTTATTL SVLLMLLF IGGSSVFNF AFIMTIG  
 ILLGLTSSLYIAPPLLL

ACTUAL ENCODED SEQUENCE

1	MVSSPILNVP	LKNHASVSGK	FTHREVSCLA	SDLKSGAMSF	VPEVLSEETI
51	SSDLGKKQCT	QCIISACCCL	AMLIVLMSVY	YRFGGVIASG	AVLLNLLLLIW
101	AALQYLDAPL	TLSGLAGIVL	AMGMAVDANV	LVFERIREEF	LLSQSLKKS
151	EKGYTAKFGA	IFDSNLTTVL	ASALLFFLDLT	GPIKGFALT	ILGIFSSMFT
201	ALFMTKFFFM	LWMNKTOHTQ	LHMMNKFVGI	KHDFLRGCKK	LWAVSGSVFL
251	LGCVALGFGA	WNSVLGMDFK	GGYAFTFNPK	EHGISDVAQM	RGKVVKHLQE
301	AGLSSRDTRI	QTFGSSEKIK	IYFSKALS	TKQIRASLLK	LTIMSWRYCG
351	IVVRNRPRFL	YGNSKRNAKF	WSKVSSKLSK	KMRYPATIGL	LGALAIILLY
401	VSLRFWEQYA	FAVCALIHD	LLATCAVLFI	AHFLLKKIQI	DLQAIGALMT
451	VLGYSLNNTL	IIFDRIREDR	QANLFTPMHV	LVNDALQKTF	SRTVMTTATT
501	LSVLLMLLFI	GGSSVFNFAP	IMTIGILLGT	LSSLYIAPPL	LLFMVRKENR
551	SK*				

Arthur

Date 20/10/20

CODING SEQUENCE

THE PROTEIN IS ENCODED ON THE POSITIVE STRAND

The ATG is presumably the start codon

The TAA is presumably the stop codon

```

1  ATGGACTTCC GCATATTGTC AGGAGGGGAT CAGCGGCACT GCTAATGGAC
51  AATATTCTGC AAACCGTGGA TGGCGTATGG CTGTAGTGAT TGACGGTTAT
101 ATGGTCAGCA GCCCTATTTT AAACGTCCCA TTGAAAAATC ATGCCAGTGT
151 CTCAGGAAAA TTTACCCACC GTGAAGTGAG CAAACTCGCC TCAGATTTAA
201 AATCTGGAGC GATGTCTTTT GTTCCCGAGG TTCTCAGTGA AGAGACGATC
251 TCTTCTGATC TTGGGAAAAA ACAATGTACA CAAGGCATTA TCTCAGCATG
301 CTGTGGCTTG GCAATGCTTA TTGTTTTGAT GAGCGTATAT TATAGATTTG
351 GAGGCGTCAT CGCTTCGGGA GCTGTTCTTC TGAATCTTTT GCTTATCTGG
401 GCAGCTCTAC AGTATTTGGA TGCGCCACTC ACCTTGTCAG GACTCGCTGG
451 GATTGTTCTT GCTATGGGGA TGGCCGTAGA TGCAAATGTT CTTGTATTCG
501 AAAGAATCCG AGAGGAATTT TTATTGTCTC AAAGTCTTAA AAAATCTGTA
551 GAAAAAGGAT ATACCAAGGC TTTTGAGGCC ATTTTGTGAT CTAAGTGGAC
601 TACAGTATTG GCCTCAGCAC TTCTTTTCTT CCTAGATACA GGGCCTATTA
651 AAGGGTTTGC TTTGACATTG ATTTTAGGAA TTTTCTCTTC AATGTTTACG
701 GCTCTTTTCA TGAATAAATT TTTCTTCATG CTGTGGATGA ATAAGACCCA
751 ACATACACAG TTGCATATGA TGAATAAGTT CGTGGGGATA AAGCATGATT
801 TCTTGAGAGG ATGCAAAAAA CTTTGGGCTG TTTCTGGAAG TGTTTTTCTT
851 TTAGGTTGCG TTGCTCTCGG GTTTGAGGCC TGAATTCCTG TTTTGGGAAT
901 GGATTTTAAA GGAGGGTATG CCTTTACCTT TAATCCAAAA GAGCATGGCA
951 TCAGCGATGT TGCTCAAATG CGTGGCAAAG TTGTGCATAA ACTACAGGAA
1001 GCTGGTCTTT CTTCTAGAGA CTTCCGTATT CAAACATTTG GATCTTCAGA
1051 AAAGATCAAA ATCTATTTTA GTGATAAAGC TTTAAGCTAT ACTAAGCAGA
1101 TACGAGCCTC TCTCCTAAAA TTAACGATCA TGAGCTGGCG TTATTGTGGG
1151 ATTGTTGTCA GAAACAGGCC TAGATTTCTC TACGGAAACT CTAAACGAAA
1201 CGCAAAATTT TGGTCAAAGG TAAGCAGCAA ACTATCGAAG AAAATGCGTT
1251 ATCAGGCGAC CATCGGGCTT TTAGGAGCTT TGGCAATCAT CTTGCTCTAT
1301 GTGAGTTTGC GCTTTGAATG GCAATATGCT TTCAGTGCCG TATGCGCTTT
1351 AATTCATGAC CTTTGGCTA CCTGTGCAGT CTTGTTTATA GCACATTTCT
1401 TTTTGAAGAA AATTCAAATA GATTTGCAAG CCATTGGTGC TTTAATGACT
1451 GTATTGGGGT ATTCATTAAA CAATACTTTG ATCATTTTGG ATCGTATTCG

```

1501 TGAAGATCGC CAAGCGAACC TGTTTACCCC TATGCATGTT TTAGTTAATG  
1551 ATGCCCTTCA AAAGACGTTC AGCCGCACGG TAATGACAAC AGCTACAAC  
1601 CTATCAGTTT TGTTAATGCT TTTGTTTATA GGCGGCTCCT CTGTCTTTAA  
1651 TTTTGCATTT ATTATGACCA TAGGGATTCT TCTAGGAAC TATCGTCTC  
1701 TTTATATTGC ACCACCTCTG TTGTTGTTTA TGGTCCGTAA AGAAAATCGC  
1751 TCAAAATAAG TACCGTTAAA CTTAATCTAA CGTGTAGCAA TATAAAAATC  
1801 TCCTTTGGGA CTTTAGTCCC AAAGGCCCT GTGGTATTAA ATTTATGACA  
1851 AATTCAGATA ATGC

# SEQUENCE ALIGNMENT

```

101 ATGGTCAGCAGCCCTATTTTAAACGTCCCATTTGAAAAATCATGCCAGTGT 150
    |||||||
    1 MetValSerSerProIleLeuAsnValProLeuLysAsnHisAlaSerVa 17

151 CTCAGGGAAATTTACCCACCGTGAAGTGAGCAAACCTCGCCTCAGATTTAA 200
    |||||||
    18 lSerGlyLysPheThrHisArgGluValSerLysLeuAlaSerAspLeuL 34

201 AATCTGGAGCGATGTCTTTTGTCTCCGAGGTTCTCAGTGAAGAGACGATC 250
    |||||||
    35 ysSerGlyAlaMetSerPheValProGluValLeuSerGluGluThrIle 50

251 TCTTCTGATCTTGGGAAAAACAATGTACACAAGGCATTATCTCAGCATG 300
    |||||||
    51 SerSerAspLeuGlyLysLysGlnCysThrGlnGlyIleIleSerAlaCy 67

301 CTGTGGCTTGGCAATGCTTATTTGTTTGTATGAGCGTATATTTATAGATTTG 350
    |||||||
    68 sCysGlyLeuAlaMetLeuIleValLeuMetSerValTyrTyrArgPheG 84

351 GAGCGCTCATCGCTTCGGGAGCTGTTCTTCTGAATCTTTTGCTTATCTGG 400
    |||||||
    85 lyGlyValIleAlaSerGlyAlaValLeuLeuAsnLeuLeuLeuIleTrp 100

401 GCAGCTCTACAGTATTTGGATGCGCCACTCACCTTGTCAGGACTCGCTGG 450
    |||||||
    101 AlaAlaLeuGlnTyrLeuAspAlaProLeuThrLeuSerGlyLeuAlaGl 117

451 GATTGTTCTTGCTATGGGGATGGCCGTAGATGCAAATGTTCTTGTATTTCG 500
    |||||||
    118 yIleValLeuAlaMetGlyMetAlaValAspAlaAsnValLeuValPheG 134

501 AAAGAATCCGAGAGGAATTTTATTGTCTCAAAGTCTTAAAAAATCTGTA 550
    |||||||
    135 luArgIleArgGluGluPheLeuLeuSerGlnSerLeuLysLysSerVal 150

551 GAAAAAGGATATACCAAGGCTTTTGGAGCCATTTTGTATTCTAACTTGAC 600
    |||||||
    151 GluLysGlyTyrThrLysAlaPheGlyAlaIlePheAspSerAsnLeuTh 167

601 TACAGTATTGGCCTCAGCACTTCTTTTCTTCTAGATACAGGGCCTATTA 650
    |||||||
    168 rThrValLeuAlaSerAlaLeuLeuPhePheLeuAspThrGlyProIleL 184

651 AAGGGTTTGCTTTGACATTGATTTTAGGAATTTCTCTTCAATGTTTACG 700
    |||||||
    185 ysGlyPheAlaLeuThrLeuIleLeuGlyIlePheSerSerMetPheThr 200

701 GCTCTTTTCATGACTAAATTTTCTTCATGCTGTGGATGAATAAGACCCA 750
    |||||||
    201 AlaLeuPheMetThrLysPhePhePheMetLeuTrpMetAsnLysThrGl 217

751 ACATACACAGTTGCATATGATGAATAAGTTCGTGGGGATAAAGCATGATT 800
    |||||||
    218 nHisThrGlnLeuHisMetMetAsnLysPheValGlyIleLysHisAspP 234

801 TCTTGAGAGGATGCAAAAAAAGCTTTGGGCTGTTTCTGGAAGTGTTTTCTT 850
    |||||||
    235 heLeuArgGlyCysLysLysLeuTrpAlaValSerGlySerValPheLeu 250

```

```

851 TTAGGTTGCGTTGCTCTCGGGTTTGGAGCCTGGAATTCCGTTTGGGAAT 900
|||||
251 LeuGlyCysValAlaLeuGlyPheGlyAlaTrpAsnSerValLeuGlyMe 267
|||||
901 GGATTTTAAAGGAGGGTATGCCTTTACCTTTAATCCAAAAGAGCATGGCA 950
|||||
268 tAspPheLysGlyGlyTyrAlaPheThrPheAsnProLysGluHisGlyI 284
|||||
951 TCAGCGATGTTGCTCAAATGCGTGGCAAAGTTGTGCATAAACTACAGGAA 1000
|||||
285 leSerAspValAlaGlnMetArgGlyLysValValHisLysLeuGlnGlu 300
|||||
1001 GCTGGTCTTTCCTCTAGAGACTTCCGTATTCAAACATTTGGATCTTCAGA 1050
|||||
301 AlaGlyLeuSerSerArgAspPheArgIleGlnThrPheGlySerSerGl 317
|||||
1051 AAAGATCAAAATCTATTTTAGTGATAAAGCTTTAAGCTATACTAAGCAGA 1100
|||||
318 uLysIleLysIleTyrPheSerAspLysAlaLeuSerTyrThrLysGlnI 334
|||||
1101 TACGAGCCTCTCTCTAAAATTAAACGATCATGAGCTGGCGTTATTGTGGG 1150
|||||
335 leArgAlaSerLeuLeuLysLeuThrIleMetSerTrpArgTyrCysGly 350
|||||
1151 ATTGTTGTCAGAAACAGGCC TAGATTTCTCTACGGAACCTCTAAACGAAA 1200
|||||
351 ileValValArgAsnArgProArgPheLeuTyrGlyAsnSerLysArgAs 367
|||||
1201 CGCAAAATTTTGGTCAAAGGTAAGCAGCAAACCTATCGAAGAAAATGCGTT 1250
|||||
368 nAlaLysPheTrpSerLysValSerSerLysLeuSerLysLysMetArgT 384
|||||
1251 ATCAGGCGACCATCGGGCTTTTAGGAGCTTTGGCAATCATCTTGCTCTAT 1300
|||||
385 yrGlnAlaThrIleGlyLeuLeuGlyAlaLeuAlaIleIleLeuLeuTyr 400
|||||
1301 GTGAGTTTGCCTTTGAATGGCAATATGCTTTTCAGTGCCGTATGCGCTTT 1350
|||||
401 ValSerLeuArgPheGluTrpGlnTyrAlaPheSerAlaValCysAlaLe 417
|||||
1351 AATTCATGACCTTTTGGCTACCTGTGCAGTCTTGTTTATAGCACATTTCT 1400
|||||
418 uIleHisAspLeuLeuAlaThrCysAlaValLeuPheIleAlaHisPheP 434
|||||
1401 TTTTGAAGAAAATTCAAATAGATTTGCAAGCCATTGGTGCTTTAATGACT 1450
|||||
435 heLeuLysLysIleGlnIleAspLeuGlnAlaIleGlyAlaLeuMetThr 450
|||||
1451 GTATTGGGGTATTCATTAAACAATACTTTGATCATTTTTGATCGTATTTCG 1500
|||||
451 ValLeuGlyTyrSerLeuAsnAsnThrLeuIleIlePheAspArgIleAr 467
|||||
1501 TGAAGATCGCCAAGCGAACCTGTTTACCCCTATGCATGTTTTAGTTAATG 1550
|||||
468 gGluAspArgGlnAlaAsnLeuPheThrProMetHisValLeuValAsnA 484
|||||
1551 ATGCCCTTCAAAAGACGTTTACGCCGACGGTAATGACAACAGCTACAAC 1600
|||||
485 spAlaLeuGlnLysThrPheSerArgThrValMetThrThrAlaThrThr 500
|||||
1601 CTATCAGTTTTGTTAATGCTTTTGTATTATAGGCGGCTCCTCTGTCTTTAA 1650
|||||
501 LeuSerValLeuLeuMetLeuLeuPheIleGlyGlySerSerValPheAs 517

```

```

1651 TTTTGCATTTATTATGACCATAGGGATTCTTCTAGGAACTTTATCGTCTC 1700
|||||
518 nPheAlaPheIleMetThrIleGlyIleLeuLeuGlyThrLeuSerSerL 534

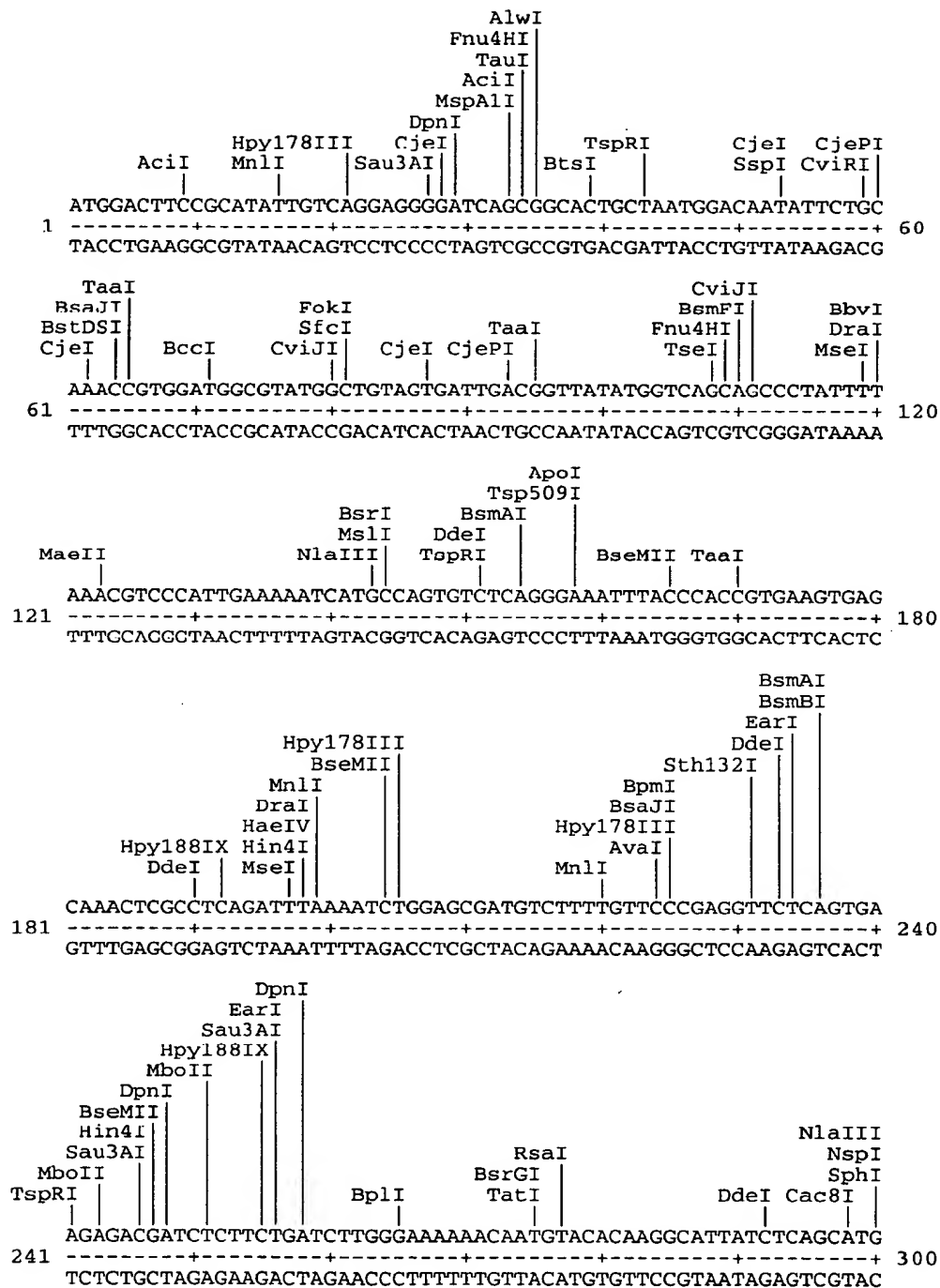
1701 TTTATATTGCACCACCTCTGTTGTTGTTTATGGTCCGTAAAGAAAATCGC 1750
|||||
535 euTyrIleAlaProProLeuLeuLeuPheMetValArgLysGluAsnArg 550

1751 TCAAAA 1756
|||||
551 SerLys 552

```



# RESTRICTION MAP



BseMII  
 CviJI  
 BsrDI  
 MnlI  
 HgaI  
 AceIII  
 Sth132I  
 Hin4I  
 BsaHI

301 CTGTGGCTTGGCAATGCTTATTGTTTTGATGAGCGTATATTATAGATTGGAGGCGTCAT  
 -----+-----+-----+-----+-----+ 360  
 GACACCGAACCCTTACGAATAACAAACTACTCGCATATAATATCTAAACCTCCGCAGTA

AceIII  
 BbvI  
 TaaI  
 SfaNI  
 SfcI  
 AluI  
 CviJI  
 Fnu4HI  
 TseI  
 CjeI  
 HinfI  
 TfiI  
 Hpy188IX  
 Hpy178III  
 MboII  
 MwoI

361 CGCTTCGGGAGCTGTTCTTCTGAATCTTTTGCTTATCTGGGCAGCTCTACAGTATTTGGA  
 -----+-----+-----+-----+-----+ 420  
 CGCAAGCCCTCGACAAGAAGACTTAGAAAACGAATAGACCCGTCGAGATGTCATAAACCT

CviJI  
 HaeIII  
 BccI  
 EaeI  
 GdiII  
 SfaNI  
 BcefI  
 HhaI  
 HphI  
 FokI  
 CjeI  
 Hpy178III  
 PleI  
 HinfI

421 TGCGCCACTCACCTTGTCAGGACTCGCTGGGATTGTTCTTGCTATGGGGA'GGCCGTAGA  
 -----+-----+-----+-----+-----+ 480  
 ACGCGGTGAGTGGAACAGTCCTGAGCGACCCTAACAAAGACGATACCCTACCGGCATCT

Hpy188IX  
 MnlI  
 ApoI  
 Tsp509I  
 BsmAI  
 MseI  
 NspV  
 HinfI  
 TfiI  
 CviRI  
 FokI

481 TGCAAATGTTCTTGTATTGCGAAAGAATCCGAGAGGAATTTTATTGTCTCAAAGTCTTAA  
 -----+-----+-----+-----+-----+ 540  
 ACGTTTACAAGAACATAAGCTTTCTTAGGCTCTCCTTAAAAATAACAGAGTTTCAGAATT

CviJI  
 BsaJI  
 StyI  
 CviJI  
 NlaIV  
 MwoI  
 HinfI  
 TfiI  
 SfcI

541 AAAATCTGTAGAAAAAGGATATACCAAGGCTTTTGGAGCCATTTTGGATTCTAACTTGAC  
 -----+-----+-----+-----+-----+ 600  
 TTTTAGACATCTTTTCTATATGGTTCCGAAAACCTCGGTAAAACTAAGATTGAACTG

BbvCI  
 Bpu10I  
 DdeI  
 CviJI  
 HaeI  
 TaaI  
 HaeIII  
 MboII  
 MnlI  
 BseMII  
 BfaI  
 EcoO109I  
 Sau96I  
 CviJI  
 HaeIII  
 EcoNI  
 MseI  
 BslI

601 TACAGTATTGGCCTCAGCACTTCTTTTCTTCCCTAGATACAGGGCTATTAAAGGGTTGTC  
 -----+-----+-----+-----+-----+ 660  
 ATGTCATAACCGGAGTCGTGAAGAAAAGAAGGATCTATGTCCCGGATAATTTCCTCAAACG

ApoI  
 Tsp509I  
 MboII  
 BceII  
 NlaIII  
 Hpy178III  
 RcaI  
 CviJI  
 EarI  
 ApoI  
 MboII  
 Tsp509I  
 TTTGACATTGATTTTAGGAATTTTCTCTTCAATGTTTACGGCTCTTTTCATGACTAAATT  
 661 ----- 720  
 AAAGTGTAACTAAAATCCTTAAAAGAGAAGTTACAAATGCCGAGAAAAGTACTGATTTAA

NdeI  
 CviRI  
 TaaI  
 SimI  
 FokI  
 NlaIII  
 XmnI  
 TTTCTTCATGCTGTGGATGAATAAGACCCAACATACACAGTTGCATATGATCAATAAGTT  
 721 ----- 780  
 AAAGAAGTACGACACCTACTTATTCTGGGTTGTATGTGTCAACGTATACTACTTATTCAA

Hpy178III  
 SmlI  
 MnlI  
 SfaNI  
 NlaIII  
 CviRI  
 Bce83I  
 FokI  
 CviJI  
 Hpy178III  
 CGTGGGGATAAAGCATGATTTCTTGAGAGGATGCAAAAAACTTTGGGCTGTTTCTGGAAG  
 781 ----- 840  
 GCACCCCTATTTTCGTACTAAAGAACTCTCCTACGTTTTTTTGAACCCGACAAAGACCTTC

ApoI  
 EcoRI  
 Tsp509I  
 ScrFI  
 CviJI  
 EcoRII  
 NlaIV  
 Sth132I  
 AvaI  
 TGTTTTTCTTTTAGGTTGCGTTGCTCTCGGGTTTGGAGCCTGGAATTCCGTTTTGGGAAT  
 841 ----- 900  
 ACAAAAAGAAAATCCAACGCAACGAGAGCCCAACCTCGGACCTTAAGGCAAAACCTTA

DraI  
 MseI  
 MnlI  
 MseI  
 NlaIII  
 SfaNI  
 GGATTTTAAAGGAGGGTATGCCTTTACCTTTAATCCAAAAGAGCATGGCATCAGCGATGT  
 901 ----- 960  
 CCTAAAAATTTCTCTCCATACGGAATGGAATTAGGTTTTCTCGTACCGTAGTCGCTACA

Hpy178III  
 BfaI  
 XbaI  
 BsmAI  
 MboII  
 AluI  
 CviJI  
 SfcI  
 CviRI  
 TGCTCAAATGCGTGGCAAAGTTGTGCATAAACTACAGGAAGCTGGTCTTTCTTTCTAGAGA  
 961 ----- 1020  
 ACGAGTTTACGCACCGTTTCAACACGTATTGATGTCCTTCGACCAGAAAGAAGATCTCT

BsaBI  
 DpnI  
 Sau3AI  
 AlwI  
 Hpy188IX

Tth111III  
 DpnI  
 BstYI  
 Sau3AI  
 Eco57I MboII  
 HindIII  
 AluI  
 CviJI  
 1021 CTTCCGTATTCAAACATTTGGATCTTCAGAAAAGATCAAAATCTATTTTAGTGATAAAGC 1080  
 -----+-----+-----+-----+-----+  
 GAAGGCATAAGTTTGTAACCTAGAAGTCTTTTCTAGTTTGTAGATAAAATCACTATTTTCG

Cac8I  
 RleAI  
 AluI  
 CviJI  
 NlaIII  
 Hpy178III  
 RcaI  
 BplI  
 DpnI  
 Sau3AI  
 MseI  
 AceIII  
 Tsp509I  
 MnlI  
 Hin4I  
 CviJI  
 DdeI  
 AluI  
 CviJI  
 MseI  
 1081 TTTAAGCTATACTAAGCAGATACGAGCCTCTCTCCTAAAATTAACGATCATGAGCTGGCG 1140  
 -----+-----+-----+-----+-----+  
 AAATTCGATATGATTTCGTCTATGCTCGGAGAGAGGATTTTAATTGCTAGTACTCGACCGC

BfaI  
 CviJI  
 HaeI  
 HaeIII  
 StuI  
 Hpy188IX  
 1141 TTATTGTGGGATTGTTGTCTAGAAACAGGCCTAGATTTCTCTACGGAAACTCTAAACGAAA 1200  
 -----+-----+-----+-----+-----+  
 AATTACACCCCTAACACAGTCTTTGTCCGATCTAAAGAGATGCCTTTGAGATTTGCTTT

BcgI  
 Fnu4HI  
 TseI  
 BbvI  
 TaqI  
 Sth132I  
 MboII  
 BcgI  
 ApoI  
 Tsp509I  
 1201 CGCAAAATTTTGGTCAAAGGTAAGCAGCAAACTATCGAAGAAAATGCGTTATCAGGCGAC 1260  
 -----+-----+-----+-----+-----+  
 GCGTTTTAAACAGTTTCCATTTCGTCGTTGATAGCTTCTTTTACGCAATAGTCCGCTG

BccI  
 CviJI  
 AluI  
 CviJI  
 HhaI  
 1261 CATCGGGCTTTTAGGAGCTTTGGCAATCATCTTGCTCTATGTGAGTTTGGCTTTGAATG 1320  
 -----+-----+-----+-----+-----+  
 GTAGCCCGAAAATCCTCGAAACCGTTAGTAGAACGAGATACACTCAAACGCGAAACTTAC

NlaIII  
 Hpy178III  
 Tsp509I  
 MseI  
 BceI  
 MwoI  
 TspRI  
 MwoI  
 HhaI  
 RcaI  
 CviJI  
 MwoI  
 CviRI  
 1321 GCAATATGCTTTTCAGTGCCGTATGCGCTTTAATTCATGACCTTTTGGCTACCTGTGCAGT 1380  
 -----+-----+-----+-----+-----+  
 CGTTATACGAAAGTCACGGCATACGCGAAATTAAGTACTGGAAAACCGATGGACACGTCA

[illegible]



>SW:SECF\_MYCTU Q50635 mycobacterium tuberculosis. protein-export membrane  
protein secf. 11/97  
Length = 442

Score = 90 (42.3 bits), Expect = 5.9e-16, Sum P(5) = 5.9e-16  
Identities = 30/118 (25%), Positives = 50/118 (42%)

Query: 316 SEKIKIYFSDKALSYTKQIRASLLKLTIMSWRXCGIVVRNRPRFLYGNSKRNAKFWSKVS 375  
SE + S T QIR+ L + + P+ G + A S VS  
Sbjct: 121 SEPQSVVIVGAGASATVQIRSETLTSDQTAKLRDALFEAFGPKGTDGQPSKQAISDSAVS 180

Query: 376 SKLSKKMRYQATIGLLGALAIILLYVSLRFQYAFSAVCALIHDLATCAVLFIHF 433  
++ +A I L+ L ++ LY+++R+E SA+ A++ DL T V + F  
Sbjct: 181 ETWGGQITKKAVIALVFLVLVALYITVRYERYMTISAITAMLFDLTVTAGVYSLVGF 238